<110> Morris, Garry P

<120> METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR EFFECTOR PEPTIDES AND RNA MOLECULES

<130> RIGL-004CON3

<140> US 09/918,601
<141> 2001-07-30

<150> US 09/727,715
<151> 2000-11-28

<150> US 08/963,368
<151> 1997-11-03

<150> US 08/589,109
<151> 1996-01-23

<150> US 08/589,911
<151> 1996-01-23

<150> US 08/789,333
<151> 1997-01-23

<150> US 08/787,738
<151> 1997-01-23

<160> 102

<170> PatentIn Ver. 2.0

<210> 1
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: random sequence.

<220>
<221> misc_feature
<222> (7)..(35)
<223> The n(s) at positions 7,8,10,11,13,14,16,17,19,20,22,23,25,26,28,29,31,32,34,35 can be any nucleic acid.

<400> 1
atgggannkn nknnknnknn knnknnknnk nnknnkgggg ggcccccc 48

<210> 2
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random sequence.

<220>
<221> VARIANT
<222> (3)..(12)
<223> The Xaa(s) at positions 3-12 can be any amino acid.

<400> 2
Met Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Pro Pro
1 5 10 15

<210> 3
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: molecular flexibility/stability sequence.

<400> 3
Gly Gly Pro Pro
1

<210> 4
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: coiled-coil structure.

<400> 4
Met Gly Cys Ala Ala Leu Glu Ser Glu Val Ser Ala Leu Glu Ser Glu
1 5 10 15

Val Ala Ser Leu Glu Ser Glu Val Ala Ala Leu Gly Arg Gly Asp Met
20 25 30

Pro Leu Ala Ala Val Lys Ser Lys Leu Ser Ala Val Lys Ser Lys Leu
35 40 45

Ala Ser Val Lys Ser Lys Leu Ala Ala Cys Gly Pro Pro
50 55 60

D1

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: loop structure.

<400> 5
Gly Arg Gly Asp Met Pro
1 5

<210> 6
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: minibody presentation structure.

<400> 6
Met Gly Arg Asn Ser Gln Ala Thr Ser Gly Phe Thr Phe Ser His Phe
1 5 10 15

Tyr Met Glu Trp Val Arg Gly Gly Glu Tyr Ile Ala Ala Ser Arg His
20 25 30

Lys His Asn Lys Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg
35 40 45

Tyr Ile Val Ser Arg Asp Thr Ser Gln Ser Ile Leu Tyr Leu Gln Lys
50 55 60

Lys Lys Gly Pro Pro
65

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear localization sequence.

<400> 7
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear loclization sequence.

<400> 8
Ala Arg Arg Arg Arg Pro
1 5

<210> 9
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear localization sequence.

<400> 9
Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear localization sequence.

<400> 10
Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5

<210> 11
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nuclear localization sequence.

<400> 11
Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
1 5 10 15

Lys Lys Leu Asp
20

<210> 12
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signal sequence.

<400> 12
Met Ala Ser Pro Leu Thr Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu
1 5 10 15

Gly Glu Ser Ile Leu Gly Ser Gly Glu Ala Lys Pro Gln Ala Pro
20 25 30

<210> 13
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signal sequence.

<400> 13
Met Ser Ser Phe Gly Tyr Arg Thr Leu Thr Val Ala Leu Phe Thr Leu
1 5 10 15

Ile Cys Cys Pro Gly
20

<210> 14
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: transmembrane domain sequence.

<400> 14
Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr
1 5 10 15

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
20 25 30

Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr
35 40 45

His Ser Arg
50

<210> 15
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: transmembrane sequence.

<400> 15
Met Val Ile Ile Val Thr Val Val Ser Val Leu Leu Ser Leu Phe Val
1 5 10 15

Thr Ser Val Leu Leu Cys Phe Ile Phe Gly Gln His Leu Arg Gln Gln
20 25 30

Arg

<210> 16
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: membrane anchor sequence.

<400> 16

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
20 25 30

Met Gly Leu Leu Thr
35

<210> 17

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:myristylation sequence.

D1

<400> 17

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg

1 5 10

<210> 18

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: palmitoylation sequence.

<400> 18

Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg Leu
20 25

<210> 19

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

D1

<223> Description of Artificial Sequence: palmitoylation sequence.

<400> 19

Lys Gln Phe Arg Asn Cys Met Leu Thr Ser Leu Cys Cys Gly Lys Asn
1 5 10 15

Pro Leu Gly Asp
20

<210> 20

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: palmitoylation sequence.

<400> 20

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

D1

<210> 21

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: lysosomal degradation sequence.

<400> 21

Lys Phe Glu Arg Gln

1 5

<210> 22

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: lysosomal membrane sequence.

<400> 22

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu

1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly

20 25 30

Tyr Gln Thr Ile

35

<210> 23

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: lysosomal degradation sequence.

<400> 23

Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
35

<210> 24

<211> 27

<212> PRT

<213> Artificial Sequence

D1

<220>

<223> Description of Artificial Sequence: mitochondrial matrix sequence.

<400> 24

Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
20 25

<210> 25

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mitochondrial inner membrane sequence.

<400> 25

Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

D1

<210> 26

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mitochondrial intermembrane sequence.

<400> 26

Met Phe Ser Met Leu Ser Lys Arg Trp Ala Gln Arg Thr Leu Ser Lys
1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
20 25 30

Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
35 40 45

Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
50 55 60

<210> 27

<211> 41

D1 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mitochondrial outer membrane sequence.

<400> 27

Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
1 5 10 15

Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
20 25 30

Gln Gln Gln Gln Gln Arg Gly Lys Lys
35 40

<210> 28

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: endoplasmic reticulum sequence.

<400> 28

Lys Asp Glu Leu
1

D1

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: endoplasmic reticulum sequence.

<400> 29

Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
1 5 10 15

<210> 30

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:farnesylation sequence.

<400> 30

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

<210> 31

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
geranylgeranylation sequence.

<400> 31

Leu Thr Glu Pro Thr Gln Pro Thr Arg Asn Gln Cys Cys Ser Asn
1 5 10 15

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:destruction
sequence.

<400> 32

Arg Thr Ala Leu Gly Asp Ile Gly Asn
1 5

<210> 33

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:secretory sequence.

<400> 33

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 34

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: secretory sequence.

<400> 34

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 35

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: secretory sequence.

<400> 35

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 36

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: secretory

sequence.

<400> 36

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 37

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:secretory
sequence.

<400> 37

Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
1 5 10 15

Cys Ala Gly Asn Phe Val His Gly
20

D1

<210> 38

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: stability sequence.

<220>

<221> VARIANT

<222> (3)..(6)

<223> The Xaa(s) at positions 3-6 can be any amino acid.

<400> 38

Met Gly Xaa Xaa Xaa Xaa Gly Gly Pro Pro
1 5 10

<210> 39

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker sequence.

D1

<400> 39

Gly Ser Gly Gly Ser
1 5

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker sequence.

<400> 40

Gly Gly Gly Ser

1

<210> 41

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

D1

<221> VARIANT

<222> (115)..(120)

<223> The Xaa(s) at postions 115-120 can be any amino acid.

<400> 41

Met Arg Pro Leu Ala Gly Gly Glu His Thr Met Ala Ser Pro Leu Thr
1 5 10 15

Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu Gly Glu Ser Ile Ile Leu
20 25 30

Gly Ser Gly Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val
35 40 45

Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
50 55 60

Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr Leu
65 70 75 80

Ile Cys Tyr His Ser Arg Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser
85 90 95

Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
100 105 110

Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Pro Pro
115 120

D1

<210> 42

<211> 173

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic.

<220>

<221> VARIANT

<222> (140)..(145)

<223> The Xaa(s) at positions 140-145 can be any amino acid.

<400> 42

Met Arg Pro Leu Ala Gly Gly Glu His Thr Met Ala Ser Pro Leu Thr
1 5 10 15

Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu Gly Glu Ser Ile Ile Leu
20 25 30

Gly Ser Gly Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val
35 40 45

Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
50 55 60

Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr Leu
65 70 75 80

Ile Cys Tyr His Ser Arg Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser

85 90 95

Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
100 105 110

Gly Gly Cys Ala Ala Leu Glu Ser Glu Val Ser Ala Leu Glu Ser Glu
115 120 125

Val Ala Ser Leu Glu Ser Glu Val Ala Ala Leu Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Leu Ala Ala Val Lys Ser Lys Leu Ser Ala Val Lys Ser Lys Leu
145 150 155 160

Ala Ser Val Lys Ser Lys Leu Ala Ala Cys Gly Pro Pro
165 170

<210> 43

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic.

D1

<220>

<221> VARIANT

<222> (38)..(43)

<223> The Xaa(s) at positions 38-43 can be any amino acid.

<400> 43

```
Met Arg Pro Leu Ala Gly Gly Glu His Thr Met Ala Ser Pro Leu Thr
 1               5                  10                  15

Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu Gly Glu Ser Ile Ile Leu
            20                  25                  30

Gly Ser Gly Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Ser Gly Gly
        35                  40                  45

Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser
    50                  55                  60

Gly Ser Gly Gly Ser Gly Gly Gly Pro Gln Arg Pro Glu Asp Cys Arg
65                  70                  75                  80

Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile
                85                  90                  95

Tyr Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser
            100                 105                 110

Leu Ile Ile Thr Leu Ile Cys Tyr His Ser Arg Gly Gly Pro Pro
        115                 120                 125
```

<210> 44

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

<221> VARIANT

<222> (63)..(68)

<223> The Xaa(s) at positions 63-68 can be any amino acid.

<400> 44

Met Arg Pro Leu Ala Gly Gly Glu His Thr Met Ala Ser Pro Leu Thr
1 5 10 15

Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu Gly Glu Ser Ile Ile Leu
20 25 30

Gly Ser Gly Gly Gly Cys Ala Ala Leu Glu Ser Glu Val Ser Ala Leu
35 40 45

Glu Ser Glu Val Ala Ser Leu Glu Ser Glu Val Ala Ala Leu Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Leu Ala Ala Val Lys Ser Lys Leu Ser Ala Val Lys
65 70 75 80

Ser Lys Leu Ala Ser Val Lys Ser Lys Leu Ala Ala Cys Gly Gly Ser
85 90 95

Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
100 105 110

Gly Ser Gly Ser Gly Gly Ser Gly Gly Gly Pro Gln Arg Pro Glu Asp
115 120 125

Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys
130 135 140

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Leu Leu
145 150 155 160

Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr His Ser Arg Gly Gly Pro
165 170 175

Pro

<210> 45

<211> 47

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

<221> VARIANT

<222> (38)..(43)

<223> The Xaa(s) at positions 38-43 can be any amino acid.

<400> 45

Met Arg Pro Leu Ala Gly Gly Glu His Arg Met Ala Ser Pro Leu Thr
1 5 10 15

Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu Gly Glu Ser Ile Ile Leu
20 25 30

Gly Ser Gly Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Pro Pro
35 40 45

<210> 46

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

D1

<220>

<221> VARIANT

<222> (62)..(67)

<223> The Xaa(s) at positions 62-67 can be any amino acid.

<400> 46

Met Arg Pro Leu Ala Gly Gly Glu His Thr Met Ala Ser Pro Leu Thr
1 5 10 15

Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu Gly Glu Ser Ile Ile Leu
20 25 30

Gly Ser Gly Gly Gly Ala Ala Leu Glu Ser Glu Val Ser Ala Leu Glu
35 40 45

Ser Glu Val Ala Ser Leu Glu Ser Glu Val Ala Ala Leu Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Leu Ala Ala Val Lys Ser Lys Leu Ser Ala Val Lys Ser
65 70 75 80

Lys Leu Ala Ser Val Lys Ser Lys Leu Ala Ala Cys Gly Pro Pro
85 90 95

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

<221> VARIANT

<222> (1)..(9)

<223> The Xaa(s) at positions 1-3, 6, 8, 9 can be any amino acid.

<400> 47

Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa

1 5

<210> 48

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

<221> misc_feature

<222> (7)..(20)

<223> The n(s) at positions 7,8,10,11,13,14,16,17,19,20 can be any nucleic acid.

<400> 48

atgggcnnkn nknnknnknn kagacctctg cctccasbkg ggsbksbkgg aggcccacct 60

taa 63

<210> 49

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

<221> VARIANT

<222> (3)..(16)

<223> The Xaa(s) at postions 3-7, 13,15,16 can be any
amino acid.

<400> 49

Met Gly Xaa Xaa Xaa Xaa Xaa Arg Pro Leu Pro Pro Xaa Pro Xaa Xaa
1 5 10 15

Gly Gly Pro Pro
20

<210> 50

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random sequence.

<220>

<221> VARIANT

<222> (2)..(11)

<223> The Xaa(s) at postions 2-11 can be any amino acid.

<400> 50

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

1 5 10

<210> 51

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: epitope tag sequence.

<400> 51

Met Gly Gly Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ser Leu

1 5 10 15

Glx

<210> 52

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PKCa translocation inhibitor sequence.

<400> 52

Gly Lys Gln Lys Thr Lys Thr Ile Lys Gly Pro Pro
1 5 10

<210> 53

<211> 92

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random sequence.

<220>

<221> misc_feature

<222> (28)..(56)

<223> The n(s) at postions

28,29,31,32,34,35,37,38,40,41,43,44,46,47,49,50,52

,53,55,56 can be any nucleic acid.

<400> 53

gcttagcaag atctctacgg tggaccknnk nnknnknnkn nknnknnknn knnknncccc 60

actcccatgg tcctacgtac caccacactg gg 92

<210> 54

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 54

gcttagcaag atctgtgtgt cagttagggt gtgg 34

<210> 55

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random

sequence.

<220>

<221> misc_feature

<222> (23)..(24)

<223> The n(s) at positions 23-24 can be any nucleic acid.

<400> 55

ctggagaacc aggaccatgg gcnnkgggcc cccttaaacc attaaat 47

<210> 56

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random sequence.

<220>

<221> misc_feature

<222> (23)..(48)

<223> The n(s) at positions 23,24,26,27,29,30,38,39,44,45,47,48 can be any nucleic acid.

<400> 56

ctggagaacc aggaccatgg gcnnknnknn kcctcccnnk cctnnknnkg ggccccctta 60

aaccattaaa t 71

<210> 57

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 57

tcatgcatcc aatttaatgg tttaag 26

<210> 58

<211> 4950

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: retroviral
vector with presentation construct sequence.

<400> 58

tgaaagaccc cacctgtagg tttggcaagc tagcttaagt aacgccattt tgcaaggcat 60

ggaaaataca taactgagaa tagagaagtt cagatcaagg ttaggaacag agagacagca 120

gaatatgggc caaacaggat atctgtggta agcagttcct gccccggctc agggccaaga 180

acagatggtc cccagatgcg gtcccgccct cagcagtttc tagagaacca tcagatgttt 240

ccagggtgcc ccaaggacct gaaaatgacc ctgtgcctta tttgaactaa ccaatcagtt 300

cgcttctcgc ttctgttcgc gcgcttctgc tccccgagct caataaaaga gcccacaacc 360

cctcactcgg cgcgccagtc ctccgataga ctgcgtcgcc cgggtacccg tattcccaat 420

aaagcctctt gctgtttgca tccgaatcgt ggactcgctg atccttggga gggtctcctc 480

agattgattg actgcccacc tcgggggtct ttcatttgga ggttccaccg agatttggag 540

accctgcct agggaccacc gacccccccg ccgggaggta agctggccag cggtcgtttc 600

ctgtctgtct ctgtctttgt gcgtgtttgt gccggcatct aatgtttgcg cctgcgtctg 660

tactagttag ctaactagct ctgtatctgg cggacccgtg gtggaactga cgagttctga 720

acacccggcc gcaaccctgg gagacgtccc agggactttg ggggccgttt ttgtggcccg 780

acctgaggaa gggagtcgat gtggaatccg accccgtcag gatatgtggt tctggtagga 840

gacgagaacc taaaacagtt cccgcctccg tctgaatttt tgctttcggt ttggaaccga 900

agccgcgcgt cttgtctgct gcagcgctgc agcatcgttc tgtgttctct ctgtctgact 960

gtgtttctgt atttgtctga aaattagggc cagactgtta ccactccctt aagtttgacc 1020

ttaggtcact ggaaagatgt cgagcggatc gctcacaacc agtcggtaga tgtcaagaag 1080

agacgttggg ttaccttctg ctctgcagaa tggccaacct ttaacgtcgg atggccgcga 1140

gacggcacct ttaaccgaga cctcatcacc caggttaaga tcaaggtctt ttcacctggc 1200

ccgcatggac acccagacca ggtcccctac atcgtgacct gggaagcctt ggcttttgac 1260

ccccctccct gggtcaagcc ctttgtacac cctaagcctc cgcctcctct tcctccatcc 1320

gccccgtctc tccccccttga acctcctcgt tcgaccccgc ctcgatcctc cctttatcca 1380

gccctcactc cttctctagg cgccggaatt ccaggaccat gggcgggccc ccttaaacca 1440

ttaaattggt aaaataaagg atccgtcgac ctgcagccaa gcttatcgat aaaataaaag 1500

attttattta gtctccagaa aaaggggga atgaaagacc ccacctgtag gtttggcaag 1560

ctagcttaag taacgccatt ttgcaaggca tggaaaatac ataactgaga atagagaagt 1620

tcagatcaag gttaggaaca gagagacagc agaatatggg ccaaacagga tatctgtggt 1680

aagcagttcc tgccccggct cagggccaag aacagatggt ccccagatgc ggtcccgccc 1740

tcagcagttt ctagagaacc atcagatgtt tccagggtgc cccaaggacc tgaaaatgac 1800

cctgtgcctt atttgaacta accaatcagt tcgcttctcg cttctgttcg cgcgcttctg 1860

ctccccgagc tcaataaaag agcccacaac ccctcactcg gcgcgccagt cctccgatag 1920

actgcgtcgc ccgggtaccc gtgtatccaa taaaccctct tgcagttgca tccgacttgt 1980

ggtctcgctg ttccttggga gggtctcctc tgagtgattg actacccgtc agcgggggtc 2040

tttcattcgt aatcatggtc atagctgttt cctgtgtgaa attgttatcc gctcacaatt 2100

ccacacaaca tacgagccgg aagcataaag tgtaaagcct ggggtgccta atgagtgagc 2160

taactcacat taattgcgtt gcgctcactg cccgctttcc agtcgggaaa cctgtcgtgc 2220

cagctgcatt aatgaatcgg ccaacgcgcg gggagaggcg gtttgcgtat tgggcgctct 2280

D1

tccgcttcct cgctcactga ctcgctgcgc tcggtcgttc ggctgcggcg agcggtatca 2340

gctcactcaa aggcggtaat acggttatcc acagaatcag gggataacgc aggaaagaac 2400

atgtgagcaa aaggccagca aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt 2460

ttccataggc tccgcccccc tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg 2520

cgaaacccga caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc 2580

tctcctgttc cgaccctgcc gcttaccgga tacctgtccg cctttctccc ttcgggaagc 2640

gtggcgcttt ctcatagctc acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc 2700

aagctgggct gtgtgcacga acccccccgtt cagcccgacc gctgcgcctt atccggtaac 2760

tatcgtcttg agtccaaccc ggtaagacac gacttatcgc cactggcagc agccactggt 2820

aacaggatta gcagagcgag gtatgtaggc ggtgctacag agttcttgaa gtggtggcct 2880

aactacggct acactagaag gacagtattt ggtatctgcg ctctgctgaa gccagttacc 2940

ttcggaaaaa gagttggtag ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt 3000

ttttttgttt gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg 3060

atcttttcta cggggtctga cgctcagtgg aacgaaaact cacgttaagg gattttggtc 3120

atgagattat caaaaaggat cttcacctag atccttttaa attaaaaatg aagttttaaa 3180

tcaatctaaa gtatatatga gtaaacttgg tctgacagtt accaatgctt aatcagtgag 3240

gcacctatct cagcgatctg tctatttcgt tcatccatag ttgcctgact ccccgtcgtg 3300

tagataacta cgatacggga gggcttacca tctggcccca gtgctgcaat gataccgcga 3360

gacccacgct caccggctcc agatttatca gcaataaacc agccagccgg aagggccgag 3420

cgcagaagtg gtcctgcaac tttatccgcc tccatccagt ctattaattg ttgccgggaa 3480

gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg ttgttgccat tgctacaggc 3540

atcgtggtgt cacgctcgtc gtttggtatg gcttcattca gctccggttc ccaacgatca 3600

aggcgagtta catgatcccc catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg 3660

atcgttgtca gaagtaagtt ggccgcagtg ttatcactca tggttatggc agcactgcat 3720

aattctctta ctgtcatgcc atccgtaaga tgcttttctg tgactggtga gtactcaacc 3780

aagtcattct gagaatagtg tatgcggcga ccgagttgct cttgcccggc gtcaatacgg 3840

gataataccg cgccacatag cagaacttta aaagtgctca tcattggaaa acgttcttcg 3900

gggcgaaaac tctcaaggat cttaccgctg ttgagatcca gttcgatgta acccactcgt 3960

gcacccaact gatcttcagc atcttttact ttcaccagcg tttctgggtg agcaaaaaca 4020

ggaaggcaaa atgccgcaaa aaagggaata agggcgacac ggaaatgttg aatactcata 4080

ctcttccttt ttcaatatta ttgaagcatt tatcagggtt attgtctcat gagcggatac 4140

atatttgaat gtatttagaa aaataaacaa atagggggttc cgcgcacatt tccccgaaaa 4200

gtgccacctg acgtctaaga aaccattatt atcatgacat taacctataa aaataggcgt 4260

atcacgaggc cctttcgtct cgcgcgtttc ggtgatgacg gtgaaaacct ctgacacatg 4320

cagctcccgg agacggtcac agcttgtctg taagcggatg ccgggagcag acaagcccgt 4380

cagggcgcgt cagcgggtgt tggcgggtgt cggggctggc ttaactatgc ggcatcagag 4440

cagattgtac tgagagtgca ccatatgcgg tgtgaaatac cgcacagatg cgtaaggaga 4500

aaataccgca tcaggcgcca ttcgccattc aggctgcgca actgttggga agggcgatcg 4560

gtgcgggcct cttcgctatt acgccagctg gcgaaagggg gatgtgctgc aaggcgatta 4620

agttgggtaa cgccagggtt ttcccagtca cgacgttgta aaacgacggc cagtgccacg 4680

ctctccctta tgcgactcct gcattaggaa gcagcccagt agtaggttga ggccgttgag 4740

caccgccgcc gcaaggaatg gtgcatgcaa ggagatggcg cccaacagtc ccccggccac 4800

ggggcctgcc accataccca cgccgaaaca agcgctcatg agcccgaagt ggcgagcccg 4860

atcttcccca tcggtgatgt cggcgatata ggcgccagca accgcacctg tggcgccggt 4920

gatgccggcc acgatgcgtc cggcgtagag 4950

<210> 59

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 59

ctggagaacc aggaccatgg gcaagagaaa gggcgatgag gtggatggag tggggccccc 60

ttaaaccatt aaat 74

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: anti-apoptosis sequence.

<400> 60

Met Gly Lys Arg Lys Gly Asp Glu Val Asp Gly Val Gly Pro Pro
1 5 10 15

<210> 61

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random sequence.

<220>

<221> misc_feature

<222> (35)..(48)

<223> The n(s) at positions 35,36,38,39,41,42,47,48 can be any nucleic acid.

<400> 61

ctggagaacc aggaccatgg gcaagagaaa gggcnnknnk nnkgaknnkg tggggccccc 60

ttaaaccatt aaat 74

<210> 62

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: random sequence.

<220>

<221> VARIANT

<222> (7)..(11)

<223> The Xaa(s) at postions 7-9,11 can be any amino acid.

<220>

<221> VARIANT

<222> (10)

<223> The amino acid at position 10 can be Aspartic acid or Glutamic acid.

D1

<400> 62

Met Gly Lys Arg Lys Gly Xaa Xaa Xaa Asp Xaa Val Gly Pro Pro

1 5 10 15

<210> 63

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 63

tcatgcatcc aatttaatgg tttaag 26

<210> 64

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 64

gatcctccct ttatccag 18

<210> 65

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 65

ctacaggtgg ggtctttc 18

<210> 66

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 66

atgggcaaga gaaagggcac ggcgtctgat gctgtggggc ccccttaa 48

<210> 67

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 67

Thr Ala Ser Asp Ala

1 5

<210> 68

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 68

atgggcaaga gaaagggcta tccttctgat gtggtggggc ccccttaa 48

<210> 69

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 69

Tyr Pro Ser Asp Val

1 5

<210> 70

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 70

atgggcaaga gaaagggcac gccttcggat atggtggggc ccccttaa 48

<210> 71

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 71

Thr Pro Ser Asp Met

1 5

<210> 72

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

D1

<400> 72

atgggcaaga gaaagggcac ggcttctgat cttgtggggc ccccttaa 48

<210> 73

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 73

Thr Ala Ser Asp Leu

1 5

<210> 74

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 74

atgggcaaga gaaagggctc tgatagggat attgtggggc ccccttaa 48

<210> 75

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 75

Ser Asp Arg Asp Ile

1 5

<210> 76

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 76

atgggcaaga gaaagggctg gttgctagag tttgtggggc ccccttaa 48

<210> 77

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 77

Trp Leu Leu Glu Phe

1 5

<210> 78

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 78

atgggcaaga gaaagggctg gttgatagag tttgtggggc ccccttaa 48

<210> 79

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 79

Trp Leu Ile Glu Phe

1 5

D1

<210> 80

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1)..(6)

<223> The Xaa(s) at positions 1-6 can be any amino acid.

<220>

<223> Description of Artificial Sequence: synthetic

<400> 80

Xaa Xaa Xaa Xaa Xaa Xaa

1 5

<210> 81

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

D1

<400> 81

Ser Tyr Gln Asp Leu

1 5

<210> 82

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<220>

<221> VARIANT

<222> (3)..(12)

<223> The Xaa(s) at positions 3-12 can be any amino acid.

<400> 82

Met Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Pro Pro
1 5 10 15

<210> 83

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 83

ctgacacaca ttccacag 18

<210> 84

<211> 122

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 84

ggatccagtg tggtggtacg taggaatacc atgggatgtc cgtctgttgc taggccgcgg 60

ggtggtgggg gccccccta gctaactaaa gatcccagtg tggtggtacg taggaattcg 120

cc 122

<210> 85

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 85

Met Gly Cys Pro Ser Val Ala Arg Pro Arg Gly Gly Gly Gly Pro Pro

1 5 10 15

<210> 86

<211> 112

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 86

ggatcccagt gtggtggtac gtaggaatac catgggattg tcttttgtta ttygtctgca 60

gcatcgtggg ggccccccct agctaactaa agatcccagt gtggtggtac gt 112

<210> 87

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 87

Met Gly Leu Ser Phe Val Ile Arg Leu Gln His Arg Gly Gly Pro Pro

1 5 10 15

<210> 88

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 88

ggatcccagt gtggtggtac gtaggagtac catgggacct ccgatttggt atactcattg 60

gagtcatggg ggccccccct agctaactaa agatcc 96

<210> 89

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 89

Met Gly Pro Pro Ile Trp Tyr Thr His Trp Ser His Gly Gly Pro Pro

1 5 10 15

<210> 90

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 90

ggatcccagt gtggtggtac gtaggagtac catggaagtc aggcgtttgt gaatactcgg 60

cataaggggg gccccccccta gctaactaaa gatcc 95

<210> 91

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 91

Met Glu Val Arg Arg Leu

1 5

<210> 92

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 92

ccggccgtat tcaacaaggg gctgaaggat gcccagaagg taccccattg tatgggatct 60

gatctggggc ctcggtgcac atgctttaca tgtgtttagt cgaggttaaa aaacgtctag 120

gccccc 126

<210> 93

<211> 107

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 93

ggatcccagt gtggtggtac gtaggaatac catgggactt tagccgggcc ccccctagct 60

aactaaagat cccagtgtgg tggtacgtag gaattcgcca gcacagt 107

<210> 94

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 94

ggatcccagt gtggtggtac gtaggaatac atgggaactg ttatggcgat gtcggattag 60

gtcgaggggg gccccccccta gctaactaaa gatcc 95

<210> 95

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 95

Met Gly Thr Val Met Ala Met Ser Asp

1 5

<210> 96

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 96

ggatccagtg tggtggtacg taggaatacc atgggatgtc cgtctgttgc taggccgcgg 60

ggtggtgggg gccccccccta gctaactaaa gatcc 95

<210> 97

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 97

Met Gly Cys Pro Ser Val Ala Arg Pro Arg Gly Gly Gly Gly Pro Pro
1 5 10 15

<210> 98

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)..(5)

<223> The Xaa(s) at postions 1-5 can be any amino acid.

<220>

<223> Description of Artificial Sequence: random sequence.

<400> 98

Xaa Xaa Xaa Xaa Xaa
1 5

<210> 99

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: histidine tag sequence.

<400> 99

His His His His His His

1 5

<210> 100

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)..(4)

<223> The Xaa(s) at postions 1-3 and 5 can be any amino acid.

<220>

<221> VARIANT

<222> (4)

<223> The amino acid at postion 4 can be Aspartic acid or Glutamic acid.

D1

<220>

<223> Description of Artificial Sequence: synthetic.

<400> 100

Xaa Xaa Xaa Asp Xaa

1 5

<210> 101

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 101

atgggcaaga gaaaaggctc ttaccaagat ctggtggggc ccccttaa 48

<210> 102

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker sequence.

<400> 102

Gly Ser

1